

4/22 #2



OIPE

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/10/016,358

DATE: 02/28/2002  
TIME: 10:27:48

Input Set : N:\Crf3\RULE60\10016358.raw.txt  
Output Set: N:\CRF3\02282002\J016358.raw

1 <110> APPLICANT: Dixon, Richard A.  
 2 Xia, Yiji  
 3 Lamb, Christopher  
 4 <120> TITLE OF INVENTION: CONSTITUTIVE DISEASE RESISTANCE (CDR1)  
 5 GENE AND METHODS OF USE THEREOF  
 6 <130> FILE REFERENCE: SALK2820-1  
 7 <140> CURRENT APPLICATION NUMBER: 10/016,358  
 8 <141> CURRENT FILING DATE: 2001-10-30  
 10 <150> PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/353,332  
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 12 <160> NUMBER OF SEQ ID NOS: 3  
 13 <170> SOFTWARE: FastSEQ for Windows Version 4.0  
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 18 <213> ORGANISM: Arabidopsis thaliana  
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 20 <221> NAME/KEY: CDS  
 21 <222> LOCATION: (1111)...(2421)  
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 25 tctgtcactt catcgaaagg acagtagaaaa aggaagatgg cttctacaaa tgccatcatt 180  
 26 gcgataaagg aaaggctatc gttcaagatg cctctaccga cagtggtccc aaagatggac 240  
 27 cccacccac gaggacatc gtggaaaaag aagacgttcc aaccacgtct tcaaagcaag 300  
 28 tggattgtat tgatataaaa gatgcgagag ttatttttt ttaattgtac tatattata 360  
 29 ttgtgtatgt tctcttaat taaaaattta tgactatata tatgacaata tatatatata 420  
 30 tatatatata tatatacatt attgagatag ataatgaata cattagttt tcattaaatt 480  
 31 taataggtac tgatcttcaa attatttca aacgattctc tgtcaatttc ttgatatttt 540  
 32 taaactaaaa tccatttttt aaaaaataga ctgatttaac aaacattaaa agttaattgt 600  
 33 ttctgtacat gccacggatc gaaaatgagt cagtaaatga atatttttt cctaaagtca 660  
 34 cacattgtat atacctaagt aaatgataca gacaaaaatt agaagatcaa gaatccttat 720  
 35 attacgaaaa tatccggta cattcggtga atacttaat gaagaatcta ggatataatt 780  
 36 aaagaagaag aaaatatgt a agcatttga aataaaataa ctggagata taagcaaacc 840  
 37 ataaaacacgt ccatatgaat gaatggtaca ctccctgtaa ataaataaaat atatccatca 900  
 38 aaatgagaaa atcttcactt ttatatttac ttaatacgtc agattctctg aacacaaaat 960  
 39 gatataattt gtagataact tactcaaaac gtaagaactc actatctatt atcatttatt 1020  
 40 aaccaccatc tcattaaatct tataaataatg tactcattag attgtcaaaa gtaaaaacctc 1080  
 41 acaatacact taaaactaca aatcaaaaaca atg gcc tct cta ttc tct tca gtt 1134  
 42 Met Ala Ser Leu Phe Ser Ser Val  
 43 1 5  
 44 ctc ttg tct ctt tgt tta ctc tct tca ctt ttt ctc tca aat gca aac 1182  
 45 Leu Leu Ser Leu Cys Leu Leu Ser Ser Leu Phe Leu Ser Asn Ala Asn

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47	gct aag cca aaa cta ggc ttc acc gcg gat cta atc cac cgt gat tct			1230
48	Ala Lys Pro Lys Leu Gly Phe Thr Ala Asp Leu Ile His Arg Asp Ser			
49	25 30 35 40			
50	cct aaa tcg ccg ttc tat aac ccg atg gaa acc tct tcc cag cgt cta			1278
51	Pro Lys Ser Pro Phe Tyr Asn Pro Met Glu Thr Ser Ser Gln Arg Leu			
52	45 50 55			
53	cga aac gcg atc cac cga tcc gtt aac cgt gtt ttc cat ttc act gaa			1326
54	Arg Asn Ala Ile His Arg Ser Val Asn Arg Val Phe His Phe Thr Glu			
55	60 65 70			
56	aag gat aac aca cca caa cca cag att gac ctc acc tca aat agc ggt			1374
57	Lys Asp Asn Thr Pro Gln Pro Ile Asp Leu Thr Ser Asn Ser Gly			
58	75 80 85			
59	gaa tat ctc atg aac gta tcc att gga aca cct ctc ttc ccg atc atg			1422
60	Glu Tyr Leu Met Asn Val Ser Ile Gly Thr Pro Pro Phe Pro Ile Met			
61	90 95 100			
62	gcc atc gcc gac acc gga agt gat ctc ctc tgg acg cag tgc gca cca			1470
63	Ala Ile Ala Asp Thr Gly Ser Asp Leu Leu Trp Thr Gln Cys Ala Pro			
64	105 110 115 120			
65	tgc gat gat tgt tac act caa gtt gat cct ctc ttt gac cct aaa acg			1518
66	Cys Asp Asp Cys Tyr Thr Gln Val Asp Pro Leu Phe Asp Pro Lys Thr			
67	125 130 135			
68	tct tcc aca tac aaa gac gtt tct tgc tcc tca agt caa tgt act gcc			1566
69	Ser Ser Thr Tyr Lys Asp Val Ser Cys Ser Ser Gln Cys Thr Ala			
70	140 145 150			
71	cta gaa aat caa gcc tct tgt tcc aca aat gac aac act tgt tct tac			1614
72	Leu Glu Asn Gln Ala Ser Cys Ser Thr Asn Asp Asn Thr Cys Ser Tyr			
73	155 160 165			
74	tca ttg tct tac ggg gat aac tca tac aca aag ggt aac atc gcc gtg			1662
75	Ser Leu Ser Tyr Gly Asp Asn Ser Tyr Thr Lys Gly Asn Ile Ala Val			
76	170 175 180			
77	gat acc tta acg ctc ggc tcc agc gat acc cgc cct atg cag ctt aag			1710
78	Asp Thr Leu Thr Leu Gly Ser Ser Asp Thr Arg Pro Met Gln Leu Lys			
79	185 190 195 200			
80	aat att att atc ggt tgt ggt cac aac aac gct gga acg ttt aac aag			1758
81	Asn Ile Ile Ile Gly Cys Gly His Asn Asn Ala Gly Thr Phe Asn Lys			
82	205 210 215			
83	aaa ggc tct gga atc gtc gga cta ggt ggt ggt ccg gtt tgc ctt atc			1806
84	Lys Gly Ser Gly Ile Val Gly Leu Gly Gly Pro Val Ser Leu Ile			
85	220 225 230			
86	aag caa ctt ggc gac tcc atc gac ggt aaa ttc tca tac tgc ttg gtt			1854
87	Lys Gln Leu Gly Asp Ser Ile Asp Gly Lys Phe Ser Tyr Cys Leu Val			
88	235 240 245			
89	cct cta act tcc aaa aag gat caa acg agt aaa atc aac ttc gga acc			1902
90	Pro Leu Thr Ser Lys Lys Asp Gln Thr Ser Lys Ile Asn Phe Gly Thr			
91	250 255 260			
92	aat gcc atc gtg tcg gga tca gga gtt gtc tca act cct ctg atc gca			1950
93	Asn Ala Ile Val Ser Gly Ser Gly Val Val Ser Thr Pro Leu Ile Ala			
94	265 270 275 280			

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95	aag gcg tct caa gag acc ttc tat tac cta acc cta aaa tcc att agc	1998
96	Lys Ala Ser Gln Glu Thr Phe Tyr Tyr Leu Thr Leu Lys Ser Ile Ser	
97	285 290 295	
98	gtg gga agc aag caa atc caa tac tca ggc tca gat tct gaa agc agc	2046
99	Val Gly Ser Lys Gln Ile Gln Tyr Ser Gly Ser Asp Ser Glu Ser Ser	
100	300 305 310	
101	gag gga aac atc atc gat tca ggc aca act tta acg tta tta ccg	2094
102	Glu Gly Asn Ile Ile Asp Ser Gly Thr Thr Leu Thr Leu Leu Pro	
103	315 320 325	
104	act gaa ttt tac tcc gag ctc gag gat gcg gtt gca tcc tct atc gat	2142
105	Thr Glu Phe Tyr Ser Glu Leu Glu Asp Ala Val Ala Ser Ser Ile Asp	
106	330 335 340	
107	gct gag aag aag caa gat cca caa agc ggt ttg agt cta tgt tac agt	2190
108	Ala Glu Lys Lys Gln Asp Pro Gln Ser Gly Leu Ser Leu Cys Tyr Ser	
109	345 350 355 360	
110	gca acc gga gat cta aaa gtt cca gtc att act atg cat ttt gat gga	2238
111	Ala Thr Gly Asp Leu Lys Val Pro Val Ile Thr Met His Phe Asp Gly	
112	365 370 375	
113	gcc gat gtg aag ctt gac tcc tcc aat gcc ttt gta caa gtc tcg gag	2286
114	Ala Asp Val Lys Leu Asp Ser Ser Asn Ala Phe Val Gln Val Ser Glu	
115	380 385 390	
116	gat ttg gtt tgc ttt gcc ttc cgc gga agc ccg agt ttc tcc ata tac	2334
117	Asp Leu Val Cys Phe Ala Phe Arg Gly Ser Pro Ser Phe Ser Ile Tyr	
118	395 400 405	
119	ggt aat gtg gcg cag atg aac ttt ctt gtt gga tac gac act gtt tcc	2382
120	Gly Asn Val Ala Gln Met Asn Phe Leu Val Gly Tyr Asp Thr Val Ser	
121	410 415 420	
122	aaa acg gtg tca ttt aag cca aca gat tgt gca aag atg tagttgttc	2431
123	Lys Thr Val Ser Phe Lys Pro Thr Asp Cys Ala Lys Met	
124	425 430 435	
125	atctcaacat gttttcaaa attgtgtttt caattacaat aatggctgat ttagttcag	2491
126	ccttagttct tttgaatttt tctaattcac atgttagtagt ctatctttc aaggagagt	2551
127	taaattctcg acctttgtt ctttgggtga tgctttgtat tcccttgaat tttcaatcac	2611
128	aattaaaatc atgaaaacct tatctccggt aactattttc ttgtccatct ctataactctg	2671
129	ttttagttta taatcatctc tatgatgtaa accaaatatg acaagacaat tctataat	2731
130	tgttcaaaat ttagttttt tttcattttt actaataaaa tctagaaata ctactttgt	2791
131	gtcttattata ttattgtat gaaataactta taagaacag atgaatgtga ttctaaattca	2851
132	atattgttt taaggaatta tattggcct actattctat ttgtatgtt tctatatttt	2911
133	actatattca atgggattat ggattataga aatattttga aatatttata ctattattta	2971
134	taaataattc aattagtttt tcttcttaag tttcttataa aaaataaaata tatcttataa	3031
135	gaaataaaata tattttatat ttcataaaaaa tcatacattg tacatatacta ggtggatgat	3091
136	acatggccta aattagatca tgaatcataa aaatccagct gtagataaaac ataacaagga	3151
137	tgaatggtac aatcctggtc aaaaaaaaaa aaaggaaaaag ttatatgcat taaaatgaga	3211
138	aaatcttcgc ttttatgtt tcttattttat cagattctct aatgttaat gacacaattt	3271
139	gtagataatt tactaaaaat gtaagaatct catcatgtac taccatttat gaatccttat	3331
140	ccaattgacc ttataaatat tactcatcag attgtaaaaa gtaaaaaactg accattcagg	3391
141	caatcactta aactacaatc taagaaaatg gcctctctat tcacttcact tctctgtct	3451
142	ctatgtttat tctcttctcc tattttctca aacgcaaacg ccaaaccaaa actaggctc	3511
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145 aatcttttgc aaaaggatgc atcacttaac gcaccacaaa ctgatatcac caaatatttc 3691
146 ggtatatac ttatgaacgt atcccttggg agttggaca cctccgtcc caatcatggc 3751
147 ggcgcgtac accggaagtg attcctatctg gacgcagtgc aaaccatgcg atgatgtta 3811
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155 gtcgggaccg ggaactgtct caactcctt ggtcgtgaag tctccagaga ccttcatttt 4291
156 tctaacccta aaatctatta ccgtggaaag caagaatatg ccaaccccaag gctctgat 4351
157 caaggaaac atggtcatcg attcgggcac aactctaact ctgttacctg ggaaatattt 4411
158 tttccagatt gagagtctg ttgcgtctt aatcgatgca gagaggctga aagatgaaag 4471
159 aatcggttcg agtcttgcata acaatgcaac cgcagatctg aaagtcccaag tcattactat 4531
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179 50 55 60
180 Asn Arg Val Phe His Phe Thr Glu Lys Asp Asn Thr Pro Gln Pro Gln
181 65 70 75 80
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183 85 90 95
184 Gly Thr Pro Pro Phe Pro Ile Met Ala Ile Ala Asp Thr Gly Ser Asp
185 100 105 110
186 Leu Leu Trp Thr Gln Cys Ala Pro Cys Asp Asp Cys Tyr Thr Gln Val
187 115 120 125
188 Asp Pro Leu Phe Asp Pro Lys Thr Ser Ser Thr Tyr Lys Asp Val Ser
189 130 135 140
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191 145 150 155 160
192 Thr Asn Asp Asn Thr Cys Ser Tyr Ser Leu Ser Tyr Gly Asp Asn Ser
193 165 170 175

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194 Tyr Thr Lys Gly Asn Ile Ala Val Asp Thr Leu Thr Leu Gly Ser Ser  
 195 180 185 190  
 196 Asp Thr Arg Pro Met Gln Leu Lys Asn Ile Ile Ile Gly Cys Gly His  
 197 195 200 205  
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 199 210 215 220  
 200 Gly Gly Gly Pro Val Ser Leu Ile Lys Gln Leu Gly Asp Ser Ile Asp  
 201 225 230 235 240  
 202 Gly Lys Phe Ser Tyr Cys Leu Val Pro Leu Thr Ser Lys Lys Asp Gln  
 203 245 250 255  
 204 Thr Ser Lys Ile Asn Phe Gly Thr Asn Ala Ile Val Ser Gly Ser Gly  
 205 260 265 270  
 206 Val Val Ser Thr Pro Leu Ile Ala Lys Ala Ser Gln Glu Thr Phe Tyr  
 207 275 280 285  
 208 Tyr Leu Thr Leu Lys Ser Ile Ser Val Gly Ser Lys Gln Ile Gln Tyr  
 209 290 295 300  
 210 Ser Gly Ser Asp Ser Glu Ser Ser Glu Gly Asn Ile Ile Ile Asp Ser  
 211 305 310 315 320  
 212 Gly Thr Thr Leu Thr Leu Leu Pro Thr Glu Phe Tyr Ser Glu Leu Glu  
 213 325 330 335  
 214 Asp Ala Val Ala Ser Ser Ile Asp Ala Glu Lys Lys Gln Asp Pro Gln  
 215 340 345 350  
 216 Ser Gly Leu Ser Leu Cys Tyr Ser Ala Thr Gly Asp Leu Lys Val Pro  
 217 355 360 365  
 218 Val Ile Thr Met His Phe Asp Gly Ala Asp Val Lys Leu Asp Ser Ser  
 219 370 375 380  
 220 Asn Ala Phe Val Gln Val Ser Glu Asp Leu Val Cys Phe Ala Phe Arg  
 221 385 390 395 400  
 222 Gly Ser Pro Ser Phe Ser Ile Tyr Gly Asn Val Ala Gln Met Asn Phe  
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VERIFICATION SUMMARY DATE: 02/28/2002  
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Input Set : N:\Crf3\RULE60\10016358.raw.txt  
Output Set: N:\CRF3\02282002\J016358.raw

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